

1/8

FIG. 1

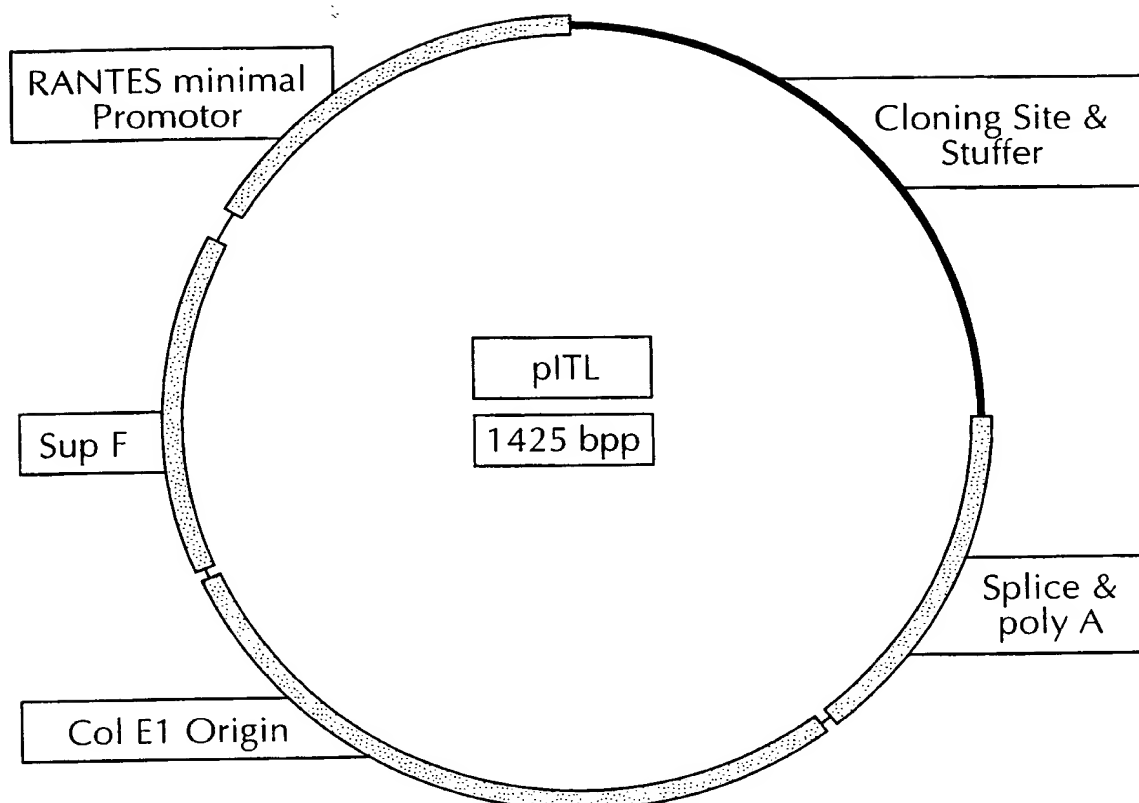
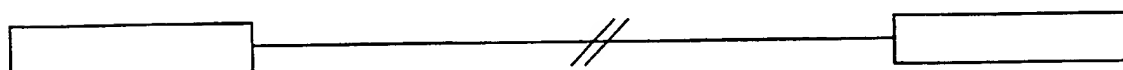


FIG. 2



GCCA/CCATGGC
CGGTGGT/ACCG

GCCT/TAAGGCG
CGGAATT/CCCG

FIG. 3A

MRPSGTAGAAALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNCCVVLGNLEITYVQRNYD
M---ELAAALCRWGLLLALLP-PGA-AST-VCTGTDMLRLPASPETHLDMLRHLVYQGCQVVOGNLELTYLPTNAS
LSFLKTIQEVAGYVLIALNTVERIPLNLQIIRGNMYENSYALAVLSNYD--AN---KT-----GLKELPMRNL
LSFLQDIOEVQGYVLIAHNQVRQVPLQRLRIVRGTLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL
QEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNHLSGCKQKDCPCNGS-CWGAGEENCQKLTKII
TEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCK-GSRCWGESSEDCQSLTRTV
CAQOCSGRCRGKSPSDCCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTPPLMLYNPTTYQMDVNPPEGKYSFGA
CAGGCA-RCKGGLPTDCCHEQCAAGCTGPKHSDCLACLFHNSHGICELHCPALVTYNTDTFESMPNPPEGRYTFGA
YVVTDHGSCVRACGADSYEME-EDGVRKCKKCEGPCRKVCNCGIGIGEFKDSL SINATNIKHFKNCTSI SGDLHLIL
YLSTDVGSC TLVCP LHNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRVTSANIQEFAGCKKIFGSLAFL
PVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQPGQFSLAVVSLNITS
PESFDGDPASNTAPLQPEQLQVFFETLEEITGYLYISAWPDSLPLDSVFQNLQVIRGRILHNGAYSLTLQGLGISW

THE 1000

3/8

FIG. 3B

LGLRSLKEISDGDV I I SGNKNLCYANTINWKKLFGTSGQKTKI ISNRGENSCKATGQVCHALCSPEGCGWGPEDRD
|||||: : | | | | : | | | | : | | | |
LGLRSLRELGSGLAIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDCEVGEGLAHQLCARGHCWGPGTGTO

475 * * * *

500

CVSCRNVSRGRECVDKCKLLEGEPRFVENSEC IQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPA
CVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQ P Q N G S V T C F G P E A D Q C V A C A H Y K D P P F C V A R C P S

[illegible]

	684	727
MRRRHIVRKRTLRLLOERELVEPLTPSGEAPNQALLRILKETEFKKIKVLGSAFGTVYKGLWIPEGEKV KIP	:	:
KRRQOKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRIKLKTELNRKVVLGSAFGTVYKGWIPDGENVKI P	: : :	: : :
	700	742

775
VAIKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMFPGCLLDYVREHKDNIGSQYLLN
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| |||
VAIKVLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMFYGCLLDHVTENRGRLGSDQLLN
790

WCVQIAKGMNYLEDVRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPICKWMALESILHRIY 850 877

WCMQIAKGMNYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEVHADGGKVPICKWMALESILRRRF 850 892

FIG. 3C

929

THQSDVWSYGVTWVELMTFGSKPYDGI PASEISSILEKGERLPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIT
:
THQSDVWSYGVTWVELMTFGAKPYDGI PA REIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPFRELVST

940

[illegible]

1000

```

-----SSPSTSRTPLLSSLATSNNSTVACIDRN--GLQSCPIKEDSFLQRYSSDPTGAL-T
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
RSSSTRSGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMAAKGLQSLPTHDPSPFLQRYSEDPTVPLPS

```

1070	E-D--SIDD	TFLP	EYINQ	-SVP	KRPA	GVQN	PVYHNQ	PLNP	APSR	DPHYQ	DPHST	AVGN	PEYLN	TVQPT	CVNS	1137
						:	:	:	:	:	:	:	:	:	:	
	ETDGY	VAPL	TCSP	QPEY	VNQD	VRPQ	PPSP	REGPL	PAAR	PAGAT	LIER	PKTL	SPGK	NGVV	KDVF	AFGG
1120	ETDGYVAPLTCSPQPEYVNQDVRPQPPSPREGPLPAARPAGATLIERPKTLSPGKNGVVKDVFAGGAVENPEYL															1290

1150
TFDSTFLPVPEYINQ-SVPKRPAGSVQNVPVYHNQLNPAPSRDPHYQDPHSTA VGNPEYLNTVQPTCVNSTFDSP
| | | | : | | : | | :
TPQGTCSPQPEYVNQPDVRPQPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAGGA VENPEYLTPQGG
1300

1210
 AHWAKGSHQ-ISL--DNPYQ-QDFFPKEAKPNIGFKGST--AENAEYLR-VAPQSSEFIGA
 AAP-QPHPPAFSPAFDNLYWDQDPPERGAPPS-TFKG-TPTAENPEYLGLDVPV
 1255

1255

FIG. 4A

57
MELAAALCRWGLLLALLPPGAASTQVCTGTMKLRLLPASPETHLDMRLHLYQGCQVQGNLELTYLPTNASLS
60
MIIMELAAWCRWGFLALLPPGIAGTQVCTGTMKLRLLPASPETHLDMRLHLYQGCQVQGNLELTYVVPANASLS

117
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTOQLFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT
120
FLQDIQEVQGYMLIAHNQVKRVPLOQLRIRIVRGTOQLFEDKYALAVLDNRDPQDNVAASTPGRTP EGLRELQRLSLT

176
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRWCGESSEDCQSLTRTVCA
180
EILKGGVLIQRNPQLCYQDMVLWKDVFRKNNQALAPVDIDTNRSRACPPCAPACKDNHCWGESPEDCQILGTICT

236
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACLFHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCV
240
SGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACLFHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCV
296
300

356
TACPYNLSTDVGSCITLVCPLHNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF
360
TTCYPYNLSTEVGSCITLVCPPNNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLRGARAITSDNVQEFDFGCKKIF

416
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPLSVFQNLQVIRGRILHNGAYSLTLQ
420
GSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYISAWPDSLRLSVFQNLRIIRGRILHNGAYSLTLQ

6/8

65 T 0 1 1 " 2 0 2 4 2 5 0

FIG. 4B

476
 GLGISWLGLRSLRELGSGLALIHNNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE-CVGEGLACHQLCARGHC
 |||||
 GLGIHSLGLRSLRELGSGLALIHNRNAHLCFVHTVPWDQLFRNPHQALLHSGNRPEEDLCVSSGLVCNSLCAHGHC
 |||||
 480
 535
 WGPGETQCVNCSQFLRGQECVEECRVLQGLPREYVNARHCLPCHPECQPONGSVTCFGPEADQCVACAHYKDPFF
 |||||
 WGPGETQCVNCSHFLLRGQECVEECRVWKGLPREYVSDKRCLPCHPECQPONSSETCFGSEADQCAACAHYKDSSS
 |||||
 540
 655
 CVARCPGKPDLSYMPIWKFPDDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIIISAVVGILLVVVLGVV
 |||||
 CVARCPGKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATVEGVLFLFLVVV
 |||||
 660
 710
 EGILI_KRR-QQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPD
 : |||||
 VGILI_KRRRQ-KIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPD
 |||||
 715
 770
 GENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPIVSRLLGICLTSTVQLVTQIMPYGCLLDHVRENRRL
 |||||
 GENVKIPVAIKVLRENTSPKANKEILDEAYVMAGVGSPIVSRLLGICLTSTVQLVTQIMPYGCLLDHVRENRRL
 |||||
 775
 830
 GSQDLNWCMIQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALE
 |||||
 GSQDLNWCMIQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDETEHADGGKVPKWMMALE
 |||||
 835
 870
 896

FIG. 4C

SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI
PAREIPDLLEKGERLPQPPICTIDVYMIMVKWMIDSECRP
SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGI
PAREIPDLLEKGERLPQPPICTIDVYMIMVKWMIDSECRP
950
955

RFRELVSEFSRMARDPQRFVVIQNE
DLGPASPLDSTFYRSLLEDDDDMGDLVDAE
EYLVPOQGFPCPDPAAGAGM
RFRELVSEFSRMARDPQRFVVIQNE
DLGPSSPMDSTFYRSLLEDDDDMGDLVDAE
EYLVPOQGFSPDPTPGTGST
1010
1015

VHHRSSSTRSGGDLTLGLEPSEEEAPR
SPLAPSEGAGSDVFDGDLGMGAAGLQSLP
THDPSPLQRYSEDPT
AHRHRSSSTRSGGDLTLGLEPSEEGP
RSPPLAPSEGAGSDVFDGDLAMGVTKGL
QSLSPHDLSPLQRYSEDPT
1070
1075

VPLPSETDGYVAPLTCSPQPEYVNQ
PDVVRPQPSPREGPLPAARPAGATLERPK
TLSPGKNGVVKDVFAFGGAVE
LPLPETDGYVAPLACSPQPEYVNQSE
VQPQPLTPEGPLPPVRPAGATLERPKTL
SPGKNGVVKDVFAFGGAVE
1130
1135
1193
1198

NPEYLTPOGGAAPQHPHPPAFSPA
FDNLYYWDQDPPERGAPSPSTFKGTPT
AENPEYLGLDVPV
NPEYLVPREGTASPPHPPAFSPA
FDNLYYWDQNSSEQPPSPNFEGTPT
AENPEYLGLDVPV
1255
1263

8/8

FIG. 5

